



SEQUENCE LISTING

<110> ..Rauch, Charles
Walczak, Henning

<120> RECEPTOR THAT BINDS TRAIL

<130> 2625-E

<140> US 09/378,045

<141> 1999-08-20

<150> US 08/883,036

<151> 1997-06-26

<150> US 08/869,852

<151> 1997-06-04

<150> US 08/829,536

<151> 1997-03-28

<150> US 08/815,255

<151> 1997-03-12

<150> US 08/799,861

<151> 1997-02-13

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 1323

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1323)

<400> 1

atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc cgg aaa	48
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys	
1 5 10 15	

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc	96
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro	
20 25 30	

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg	144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu	
35 40 45	

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag	192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln	
50 55 60	

cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg	240
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu	
65 70 75 80	

tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc	288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser	
85 90 95	
tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc	336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe	
100 105 110	
tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg	384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro	
115 120 125	
tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc	432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe	
130 135 140	
cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt	480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys	
145 150 155 160	
ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc	528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile	
165 170 175	
gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca	576
Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro	
180 185 190	
gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc	624
Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro	
195 200 205	
tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc	672
Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val	
210 215 220	
ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc	720
Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val	
225 230 235 240	
ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag	768
Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu	
245 250 255	
cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc	816
Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu	
260 265 270	
aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa	864
Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu	
275 280 285	
atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc	912
Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser	
290 295 300	
ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct	960
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser	
305 310 315 320	

cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag	1008
Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu	
325 330 335	
act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac	1056
Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp	
340 345 350	
tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata	1104
Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile	
355 360 365	
aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg	1152
Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr	
370 375 380	
atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac	1200
Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His	
385 390 395 400	
acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag	1248
Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln	
405 410 415	
aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa	1296
Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu	
420 425 430	
ggg aat gca gac tct gcc atg tcc taa	1323
Gly Asn Ala Asp Ser Ala Met Ser	
435 440	

<210> 2
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1 5 10 15
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
20 25 30
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
35 40 45
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
50 55 60
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65 70 75 80
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser

85					90					95					
Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	Trp	Asn	Asp	Leu	Leu	Phe
			100					105					110		
Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro
		115					120					125			
Cys	Thr	Thr	Thr	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe
	130					135					140				
Arg	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys
145					150					155					160
Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile
				165					170					175	
Glu	Cys	Val	His	Lys	Glu	Ser	Gly	Thr	Lys	His	Ser	Gly	Glu	Ala	Pro
			180					185					190		
Ala	Val	Glu	Glu	Thr	Val	Thr	Ser	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Pro
		195					200					205			
Cys	Ser	Leu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val
	210					215					220				
Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	Val
225					230					235					240
Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	Pro	Glu
				245					250					255	
Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	Asn	Val	Leu
			260					265					270		
Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu
		275					280					285			
Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser
	290					295					300				
Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	Glu	Arg	Ser
305					310					315					320
Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Glu	Gly	Asp	Pro	Thr	Glu
				325					330					335	

Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
 340 345 350

Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
 355 360 365

Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
 370 375 380

Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
 385 390 395 400

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
 405 410 415

Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
 420 425 430

Gly Asn Ala Asp Ser Ala Met Ser
 435 440

<210> 3
 <211> 157
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (3)..(155)

<220>
 <221> misc_feature
 <222> (145)..(145)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (149)..(149)
 <223> n is a, c, g, or t

<400> 3
 ct gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc 47
 Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro
 1 5 10 15

ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat 95
 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn
 20 25 30

gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg 143
 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu

35 40 45 157

tnc acn atg ctg at
 Xaa Thr Met Leu
 50

<210> 4
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (48)..(48)
 <223> The 'Xaa' at location 48 stands for Tyr, Cys, Ser, or Phe.

<400> 4

Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe
 1 5 10 15

Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu
 20 25 30

Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa
 35 40 45

Thr Met Leu
 50

<210> 5
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG peptide

<400> 5

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 6
 <211> 3159
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Cloning Vector pGP1k

<400> 6
 aattagcggc cgctgtcgac aagcttcgaa ttcagtatcg atgtggggta cctactgtcc 60

cgggattgcg gatccgcgat gatatcgttg atcctcgagt gcggccgcag tatgcaaaaa 120

aaagcccgct cattaggcgg gctcttggca gaacatatcc atcgcggtccg ccatctccag	180
dagccgcacg cggcgcatct cgggcagcgt tgggtcctgg ccacgggtgc gcatgatcgt	240
gctcctgtcg ttgaggaccc ggctaggctg gcgggggttg cttactgggt agcagaatga	300
atcaccgata cgcgagcgaa cgtgaagcga ctgctgctgc aaaacgtctg cgacctgagc	360
aacaacatga atggtcttcg gtttccgtgt ttcgtaaagt ctggaaacgc ggaagtcagc	420
gccctgcacc attatgttcc ggatctgcat cgcaggatgc tgctggctac cctgtggaac	480
acctacatct gtattaacga agcgtctggca ttgacctga gtgatttttc tctgggtccc	540
ccgcatccat accgccagtt gtttaccctc acaacgttcc agtaaccggg catgttcac	600
atcagtaacc cgtatcgtga gcatcctctc tcgtttcatc ggtatcatta ccccatgaa	660
cagaaattcc cccttacacg gaggcacaa gtgaccaaac agggaaaaac cgcccttaac	720
atggcccgcgt ttatcagaag ccagacatta acgcttctgg agaaactcaa cgagctggac	780
gcggatgaac aggcagacat ctgtgaatcg cttcacgacc acgctgatga gctttaccgc	840
agctgcctcg cgcgtttcgg tgatgacggg gaaaacctct gacacatgca gctcccggag	900
acggtcacag cttgtctgta agcggatgcc gggagcagac aagcccgtca gggcgcgtca	960
gcgggtgttg gcgggtgtcg gggcgagcc atgaccagc cacgtagcga tagcggagt	1020
tatactgggt taactatgcg gcatcagagc agattgtact gagagtgcac catatgcgg	1080
gtgaaatacc gcacagatgc gtaaggagaa aataccgcac caggcgctct tccgcttcct	1140
cgtcactga ctcgctgcgc tcggtcgttc ggctgcggcg agcggtatca gctcactcaa	1200
aggcggtaat acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa	1260
aaggccagca aaaggccagg aaccgtaaaa aggcgcggtt gctggcggtt ttccataggc	1320
tccgcccccc tgacgagcat caaaaaatc gacgtcaag tcagaggtgg cgaaaccgca	1380
caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc	1440
cgacctgcc gcttaccgga tacctgtccg cttttctccc ttcgggaagc gtggcgcttt	1500
ctcatagctc acgctgtagg tatctcagtt cgggtgtaggt cgttcgctcc aagctgggct	1560
gtgtgcacga acccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg	1620
agtccaaccc ggtaagacac gacttatcgc cactggcagc agccaggcgc gccttggcct	1680
aagaggccac tggtaacagg attagcagag cgaggatatgt aggcggtgct acagagttct	1740
tgaagtgggtg gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc	1800
tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg	1860
ctggtagcgg tgggtttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc	1920

aagaagatcc	tttgatcttt	tctacggggt	ctgacgctca	gtggaacgaa	aactcacgtt	1980
aagggatttt	ggtcattgaga	ttatcaaaaa	ggatcttcac	ctagatcctt	ttaaattaaa	2040
aatgaagttt	taaatcaatc	taaagtatat	atgagtaaac	ttggtctgac	agttaccaat	2100
gcttaatcag	tgaggcacct	atctcagcga	tctgtctatt	tcgttcatcc	atagttgcct	2160
gactccccgt	cgtgtagata	actacgatac	gggaggggctt	accatctggc	cccagtgctg	2220
caatgatacc	gcgagacca	cgctcaccgg	ctccagattt	atcagcaata	aaccagccag	2280
ccggaagggc	cgagcgcaga	agtggctctg	caactttatc	cgctccatc	cagtctatta	2340
attgttgccg	ggaagctaga	gtaagtagtt	cgccagttaa	tagtttgccg	aacgttggtg	2400
ccattgctgc	aggcatcgtg	gtgtcacgct	cgtcgtttgg	tatggcttca	ttcagctccg	2460
gttcccaacg	atcaaggcga	gttacatgat	ccccatggt	gtgcaaaaaa	gcggttagct	2520
ccttcgggtc	tccgatcgtt	gtcagaagta	agttggccgc	agtgttatca	ctcatggtta	2580
tggcagcact	gcataattct	cttactgtca	tgccatccgt	aagatgcttt	tctgtgactg	2640
gtgagtactc	aaccaagtca	ttctgagaat	agtgtatgcg	gcgaccgagt	tgctcttgcc	2700
cggcgtcaac	acgggataat	accgcgccac	atagcagaac	tttaaaagtg	ctcatcattg	2760
gaaaacgttc	ttcggggcga	aaactctcaa	ggatcttacc	gctgttgaga	tccagttcga	2820
tgtaaccac	tcgtgcaccc	aactgatctt	cagcatcttt	tactttcacc	agcgtttctg	2880
ggtgagcaaa	aacaggaagg	caaatgccc	caaaaaaggg	aataagggcg	acacggaaat	2940
gttgaatact	catactcttc	ctttttcaat	attattgaag	catttatcag	ggttattgtc	3000
tcattgagcgg	atacatattt	gaatgtattt	agaaaaataa	acaaataggg	gttccgcgca	3060
catttccccg	aaaagtgcc	cctgacgtct	aagaaacat	tattatcatg	acattaacct	3120
ataaaaatag	gcgtatcacg	aggccctttc	gtcttcaag			3159